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<!--StartFragment-->RESULT 4
AAQ28389
ID    AAQ28389 standard; DNA; 2907 BP.
XX
AC    AAQ28389;
XX
DT    27-AUG-2003  (revised)
DT    25-MAR-2003  (revised)
DT    12-FEB-1993  (first entry)
XX
DE    Gene from the ALS mutant of Arapidopsis.
XX
KW    Herbicide resistant; acetolactate synthase; ALS; sulphonylurea;
KW    triazolopyrimidinesulphonamide; imidazolinone; markers; ss.
XX
OS    Arabidopsis thaliana.
XX
FH    Key               Location/Qualifiers
FT    CDS               506. .2518
FT                      /*tag=  a
XX
PN    US5141870-A.
XX
PD    25-AUG-1992.
XX
PF    18-JAN-1991;   91US-00642976.
XX
PR    26-AUG-1986;   86US-00900609.
PR    04-MAR-1988;   88US-00164360.
XX
PA    (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI    Bedbrook JR,  Chaleff RS,  Falco SC,  Mazur BJ,  Somerville CR;
PI    Yadav NS;
XX
DR    WPI; 1992-307863/37.
DR    P-PSDB; AAR26913.
XX
PT    Conferring herbicide resistance on plants - using a nucleic acid fragment
PT    encoding a herbicide-resistant plant aceto:lactate synthase protein.
XX
PS    Disclosure; Fig 10; 63pp; English.
XX
CC    The DNA sequence is that of a mutant acetolactate synthetase gene
CC    isolated from herbicide resistant strains of Arabidopsis thaliana.
CC    designated GH50. The GH50 mutant ALS gene may be isolated from
CC    Arapidopsis plants resistant to sulphonylurea, triazolopyrimidine
CC    sulphonamide and imidazolinone herbicides. The gene may be used to
CC    transform plants to confer herbicide resistance to plants such as
CC    tobacco, petunia, cotton, sugarbeet, potato, tomato, lettuce, sunflower,
CC    soybean, corn, wheat, rice, poplars, alfalfa, oats, etc. The herbicide
CC    resistant ALS genes can also be used as markers for transformation of an
CC    organism by a second DNA fragment. See also AAQ28387-8. (Updated on 25-
CC    MAR-2003 to correct PF field.) (Updated on 27-AUG-2003 to correct OS
CC    field.)
XX
SQ    Sequence 2907 BP; 757 A; 610 C; 636 G; 904 T; 0 U; 0 Other;

  Query Match              50.8%;   Score 2903.8;   DB 2;   Length 2907;
  Best Local Similarity    99.9%;   Pred. No. 0;
  Matches 2905;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy    1979  GCTCTTAGTTTTGTTATTGTTTTTGTAGCCAAATTCTCCATTCTTATTCCATTTTCACTT  2038
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1  GCTCTTAGTTTTGTTATTGTTTTTGTAGCCAAATTCTCCATTCTTATTCCATTTTCACTT    60

Qy    2039  ATCTCTTGTTCCTTATAGACCTTATAAGTTTTTTATTCATGTATACAAATTATATTGTCA  2098
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  ATCTCTTGTTCCTTATAGACCTTATAAGTTTTTTATTCATGTATACAAATTATATTGTCA   120

Qy    2099  TCAAGAAGTATCTTTAAAATCTAAATCTCAAATCACCAGGACTATGTTTTTGTCCAATTC  2158
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  TCAAGAAGTATCTTTAAAATCTAAATCTCAAATCACCAGGACTATGTTTTTGTCCAATTC   180

Qy    2159  GTGGAACCAACTTGCAGCTTGTATCCATTCTCTTAACCAATAAAAAAAGAAAGAAAGATC  2218
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  GTGGAACCAACTTGCAGCTTGTATCCATTCTCTTAACCAATAAAAAAAGAAAGAAAGATC   240

Qy    2219  AATTTGATAAATTTCTCAGCCACAAATTCTACATTTAGGTTTTAGCATATCGAAGGCTCA  2278
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  AATTTGATAAATTTCTCAGCCACAAATTCTACATTTAGGTTTTAGCATATCGAAGGCTCA   300

Qy    2279  ATCACAAATACAATAGATAGACTAGAGATTCCAGCGTCACGTGAGTTTTATCTATAAATA  2338
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  ATCACAAATACAATAGATAGACTAGAGATTCCAGCGTCACGTGAGTTTTATCTATAAATA   360

Qy    2339  AAGGACCAAAAATCAAATCCCGAGGGCATTTTCGTAATCCAACATAAAACCCTTAAACTT  2398
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  AAGGACCAAAAATCAAATCCCGAGGGCATTTTCGTAATCCAACATAAAACCCTTAAACTT   420

Qy    2399  CAAGTCTCATTTTTAAACAAATCATGTTCACAAGTCTCTTCTTCTTCTCTGTTTCTCTAT  2458
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  CAAGTCTCATTTTTAAACAAATCATGTTCACAAGTCTCTTCTTCTTCTCTGTTTCTCTAT   480

Qy    2459  CTCTTGCTCATCTTTCTCCTGAACCATGGCGGCGGCAACAACAACAACAACAACATCTTC  2518
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  CTCTTGCTCATCTTTCTCCTGAACCATGGCGGCGGCAACAACAACAACAACAACATCTTC   540

Qy    2519  TTCGATCTCCTTCTCCACCAAACCATCTCCTTCCTCCTCCAAATCACCATTACCAATCTC  2578
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  TTCGATCTCCTTCTCCACCAAACCATCTCCTTCCTCCTCCAAATCACCATTACCAATCTC   600

Qy    2579  CAGATTCTCCCTCCCATTCTCCCTAAACCCCAACAAATCATCCTCCTCCTCCCGCCGCCG  2638
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  CAGATTCTCCCTCCCATTCTCCCTAAACCCCAACAAATCATCCTCCTCCTCCCGCCGCCG   660

Qy    2639  CGGTATCAAATCCAGCTCTCCCTCCTCCATCTCCGCCGTGCTCAACACAACCACCAATGT  2698
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  CGGTATCAAATCCAGCTCTCCCTCCTCCATCTCCGCCGTGCTCAACACAACCACCAATGT   720

Qy    2699  CACAACCACTCCCTCTCCAACCAAACCTACCAAACCCGAAACATTCATCTCCCGATTCGC  2758
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  CACAACCACTCCCTCTCCAACCAAACCTACCAAACCCGAAACATTCATCTCCCGATTCGC   780

Qy    2759  TCCAGATCAACCCCGCAAAGGCGCTGATATCCTCGTCGAAGCTTTAGAACGTCAAGGCGT  2818
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  TCCAGATCAACCCCGCAAAGGCGCTGATATCCTCGTCGAAGCTTTAGAACGTCAAGGCGT   840

Qy    2819  AGAAACCGTATTCGCTTACCCTGGAGGTGCATCAATGGAGATTCACCAAGCCTTAACCCG  2878
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  AGAAACCGTATTCGCTTACCCTGGAGGTGCATCAATGGAGATTCACCAAGCCTTAACCCG   900
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Qy    2879  CTCTTCCTCAATCCGTAACGTCCTTCCTCGTCACGAACAAGGAGGTGTATTCGCAGCAGA  2938
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  CTCTTCCTCAATCCGTAACGTCCTTCCTCGTCACGAACAAGGAGGTGTATTCGCAGCAGA   960

Qy    2939  AGGATACGCTCGATCCTCAGGTAAACCAGGTATCTGTATAGCCACTTCAGGTCCCGGAGC  2998
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  AGGATACGCTCGATCCTCAGGTAAACCAGGTATCTGTATAGCCACTTCAGGTCCCGGAGC  1020

Qy    2999  TACAAATCTCGTTAGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCAAT  3058
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  TACAAATCTCGTTAGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCAAT  1080

Qy    3059  CACAGGACAAGTCCCTCGTCGTATGATTGGTACAGATGCGTTTCAAGAGACTCCGATTGT  3118
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  CACAGGACAAGTCTCTCGTCGTATGATTGGTACAGATGCGTTTCAAGAGACTCCGATTGT  1140

Qy    3119  TGAGGTAACGCGTTCGATTACGAAGCATAACTATCTTGTGATGGATGTTGAAGATATCCC  3178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  TGAGGTAACGCGTTCGATTACGAAGCATAACTATCTTGTGATGGATGTTGAAGATATCCC  1200

Qy    3179  TAGGATTATTGAGGAAGCTTTCTTTTTAGCTACTTCTGGTAGACCTGGACCTGTTTTGGT  3238
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  TAGGATTATTGAGGAAGCTTTCTTTTTAGCTACTTCTGGTAGACCTGGACCTGTTTTGGT  1260

Qy    3239  TGATGTTCCTAAAGATATTCAACAACAGCTTGCGATTCCTAATTGGGAACAGGCTATGAG  3298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261  TGATGTTCCTAAAGATATTCAACAACAGCTTGCGATTCCTAATTGGGAACAGGCTATGAG  1320

Qy    3299  ATTACCTGGTTATATGTCTAGGATGCCTAAACCTCCGGAAGATTCTCATTTGGAGCAGAT  3358
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321  ATTACCTGGTTATATGTCTAGGATGCCTAAACCTCCGGAAGATTCTCATTTGGAGCAGAT  1380

Qy    3359  TGTTAGGTTGATTTCTGAGTCTAAGAAGCCTGTGTTGTATGTTGGTGGTGGTTGTTTGAA  3418
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381  TGTTAGGTTGATTTCTGAGTCTAAGAAGCCTGTGTTGTATGTTGGTGGTGGTTGTTTGAA  1440

Qy    3419  TTCTAGCGATGAATTGGGTAGGTTTGTTGAGCTTACGGGGATCCCTGTTGCGAGTACGTT  3478
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441  TTCTAGCGATGAATTGGGTAGGTTTGTTGAGCTTACGGGGATCCCTGTTGCGAGTACGTT  1500

Qy    3479  GATGGGGCTGGGATCTTATCCTTGTGATGATGAGTTGTCGTTACATATGCTTGGAATGCA  3538
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501  GATGGGGCTGGGATCTTATCCTTGTGATGATGAGTTGTCGTTACATATGCTTGGAATGCA  1560

Qy    3539  TGGGACTGTGTATGCAAATTACGCTGTGGAGCATAGTGATTTGTTGTTGGCGTTTGGGGT  3598
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561  TGGGACTGTGTATGCAAATTACGCTGTGGAGCATAGTGATTTGTTGTTGGCGTTTGGGGT  1620

Qy    3599  AAGGTTTGATGATCGTGTCACGGGTAAGCTTGAGGCTTTTGCTAGTAGGGCTAAGATTGT  3658
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621  AAGGTTTGATGATCGTGTCACGGGTAAGCTTGAGGCTTTTGCTAGTAGGGCTAAGATTGT  1680

Qy    3659  TCATATTGATATTGACTCGGCTGAGATTGGGAAGAATAAGACTCCTCATGTGTCTGTGTG  3718
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681  TCATATTGATATTGACTCGGCTGAGATTGGGAAGAATAAGACTCCTCATGTGTCTGTGTG  1740

Qy    3719  TGGTGATGTTAAGCTGGCTTTGCAAGGGATGAATAAGGTTCTTGAGAACCGAGCGGAGGA  3778
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741  TGGTGATGTTAAGCTGGCTTTGCAAGGGATGAATAAGGTTCTTGAGAACCGAGCGGAGGA  1800

Qy    3779  GCTTAAGCTTGATTTTGGAGTTTGGAGGAATGAGTTGAACGTACAGAAACAGAAGTTTCC  3838
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Db    1801    GCTTAAGCTTGATTTTGGAGTTTGGAGGAATGAGTTGAACGTACAGAAACAGAAGTTTCC  1860

Qy    3839    GTTGAGCTTTAAGACGTTTGGGGAAGCTATTCCTCCACAGTATGCGATTAAGGTCCTTGA  3898
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1861    GTTGAGCTTTAAGACGTTTGGGGAAGCTATTCCTCCACAGTATGCGATTAAGGTCCTTGA  1920

Qy    3899    TGAGTTGACTGATGGAAAAGCCATAATAAGTACTGGTGTCGGGCAACATCAAATGTGGGC  3958
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1921    TGAGTTGACTGATGGAAAAGCCATAATAAGTACTGGTGTCGGGCAACATCAAATGTGGGC  1980

Qy    3959    GGCGCAGTTCTACAATTACAAGAAACCAAGGCAGTGGCTATCATCAGGAGGCCTTGGAGC  4018
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1981    GGCGCAGTTCTACAATTACAAGAAACCAAGGCAGTGGCTATCATCAGGAGGCCTTGGAGC  2040

Qy    4019    TATGGGATTTGGACTTCCTGCTGCGATTGGAGCGTCTGTTGCTAACCCTGATGCGATAGT  4078
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2041    TATGGGATTTGGACTTCCTGCTGCGATTGGAGCGTCTGTTGCTAACCCTGATGCGATAGT  2100

Qy    4079    TGTGGATATTGACGGAGATGGAAGCTTTATAATGAATGTGCAAGAGCTAGCCACTATTCG  4138
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2101    TGTGGATATTGACGGAGATGGAAGCTTTATAATGAATGTGCAAGAGCTAGCCACTATTCG  2160

Qy    4139    TGTAGAGAATCTTCCAGTGAAGGTACTTTTATTAAACAACCAGCATCTTGGCATGGTTAT  4198
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2161    TGTAGAGAATCTTCCAGTGAAGGTACTTTTATTAAACAACCAGCATCTTGGCATGGTTAT  2220

Qy    4199    GCAATGGGAAGATCGGTTCTACAAAGCTAACCGAGCTCACACATTTCTCGGGGATCCGGC  4258
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2221    GCAATGGGAAGATCGGTTCTACAAAGCTAACCGAGCTCACACATTTCTCGGGGATCCGGC  2280

Qy    4259    TCAGGAGGACGAGATATTCCCGAACATGTTGCTGTTTGCAGCAGCTTGCGGGATTCCAGC  4318
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2281    TCAGGAGGACGAGATATTCCCGAACATGTTGCTGTTTGCAGCAGCTTGCGGGATTCCAGC  2340

Qy    4319    GGCGAGGGTGACAAAGAAAGCAGATCTCCGAGAAGCTATTCAGACAATGCTGGATACACC  4378
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2341    GGCGAGGGTGACAAAGAAAGCAGATCTCCGAGAAGCTATTCAGACAATGCTGGATACACC  2400

Qy    4379    AGGACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGTTGCCGATGATCCC  4438
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2401    AGGACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGTTGCCGATGATCCC  2460

Qy    4439    GAATGGTGGCACTTTCAACGATGTCATAACGGAAGGAGATGGCCGGATTAAATACTGAGA  4498
              | |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2461    GAGTGGTGGCACTTTCAACGATGTCATAACGGAAGGAGATGGCCGGATTAAATACTGAGA  2520

Qy    4499    GATGAAACCGGTGATTATCAGAACCTTTTATGGTCTTTGTATGCATATGGTAAAAAAACT  4558
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2521    GATGAAACCGGTGATTATCAGAACCTTTTATGGTCTTTGTATGCATATGGTAAAAAAACT  2580

Qy    4559    TAGTTTGCAATTTCCTGTTTGTTTTGGTAATTTGAGTTTCTTTTAGTTGTTGATCTGCCT  4618
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2581    TAGTTTGCAATTTCCTGTTTGTTTTGGTAATTTGAGTTTCTTTTAGTTGTTGATCTGCCT  2640

Qy    4619    GCTTTTTGGTTTACGTCAGACTACTACTGCTGTTGTTGTTTGGTTTCCTTTCTTTCATTT  4678
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2641    GCTTTTTGGTTTACGTCAGACTACTACTGCTGTTGTTGTTTGGTTTCCTTTCTTTCATTT  2700

Qy    4679    TATAAATAAATAATCCGGTTCGGTTTACTCCTTGTGACTGGCTCAGTTTGGTTATTGCGA  4738
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db       2701 TATAAATAAATAATCCGGTTCGGTTTACTCCTTGTGACTGGCTCAGTTTGGTTATTGCGA 2760

Qy       4739 AATGCGAATGGTAAATTGAGTAATTGAAATTCGTTATTAGGGTTCTAAGCTGTTTTAACA 4798
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 AATGCGAATGGTAAATTGAGTAATTGAAATTCGTTATTAGGGTTCTAAGCTGTTTTAACA 2820

Qy       4799 GTCACTGGGTTAATATCTCTCGAATCTTGCATGGAAAATGCTCTTACCATTGGTTTTTAA 4858
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GTCACTGGGTTAATATCTCTCGAATCTTGCATGGAAAATGCTCTTACCATTGGTTTTTAA 2880

Qy       4859 TTGAAATGTGCTCATATGGGCCGTGGT 4885
              |||||||||||||||||||||||||||
Db       2881 TTGAAATGTGCTCATATGGGCCGTGGT 2907
<!--EndFragment-->
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